

SEQUENCE LISTING

<110> Merck & Co., Inc.
LaMonica, Nicola
Facciabene, Andrea
Aurismicchio, Luigi

<120> CARCINOEMBRYONIC ANTIGEN FUSIONS AND
USES THEREOF

<130> ITR0073YP

<150> PCT/EP2005/001114

<151> 2005-02-03

<150> 60/635,791

<151> 2004-12-14

<150> 60/543,649

<151> 2004-02-11

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<213> Artificial Sequence

<220>

<223> PCR Primer

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<210> 7

<211> 2766

<212> DNA

<213> Artificial Sequence

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<223> CEA-LTA fusion

<400> 7

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taccgggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgtg ggaggacaag 480
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ttatga

2766

<210> 8

<211> 921

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 8

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Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      35             40             45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
      50             55             60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65             70             75             80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
      85             90             95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
      100            105            110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
      115            120            125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130            135            140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145            150            155            160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
      165            170            175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
      180            185            190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
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Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
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Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
                      245                      250                      255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
                      260                      265                      270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
                      275                      280                      285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290                      295                      300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305                      310                      315                      320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                      325                      330                      335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
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Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
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Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370                      375                      380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385                      390                      395                      400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                      405                      410                      415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
                      420                      425                      430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
                      435                      440                      445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450                      455                      460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                      470                      475                      480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
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Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro

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Pro Arg Leu Gln Leu Ser Asn	Gly Asn Arg Thr Leu Thr	Leu Phe Asn
545	550	555
Val Thr Arg Asn Asp Ala Arg	Ala Tyr Val Cys Gly Ile	Gln Asn Ser
565	570	575
Val Ser Ala Asn Arg Ser Asp	Pro Val Thr Leu Asp Val	Leu Tyr Gly
580	585	590
Pro Asp Thr Pro Ile Ile Ser	Pro Pro Asp Ser Ser Tyr	Leu Ser Gly
595	600	605
Ala Asn Leu Asn Leu Ser Cys	His Ser Ala Ser Asn Pro	Ser Pro Gln
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Tyr Ser Trp Arg Ile Asn Gly	Ile Pro Gln Gln His Thr	Gln Val Leu
625	630	635
Phe Ile Ala Lys Ile Thr Pro	Asn Asn Asn Gly Thr Tyr	Ala Cys Phe
645	650	655
Val Ser Asn Leu Ala Thr Gly	Arg Asn Asn Ser Ile Val	Lys Ser Ile
660	665	670
Thr Val Ser Ala Ser Gly Thr	Leu Val Asn Gly Asp Lys	Leu Tyr Arg
675	680	685
Ala Asp Ser Arg Pro Pro Asp	Glu Ile Lys Arg Ser Gly	Gly Leu Met
690	695	700
Pro Arg Gly His Asn Glu Tyr	Phe Asp Arg Gly Thr Gln	Met Asn Ile
705	710	715
Asn Leu Tyr Asp His Ala Arg	Gly Thr Gln Thr Gly Phe	Val Arg Tyr
725	730	735
Asp Asp Gly Tyr Val Ser Thr	Ser Leu Ser Leu Arg Ser	Ala His Leu
740	745	750
Ala Gly Gln Ser Ile Leu Ser	Gly Tyr Ser Thr Tyr Tyr	Ile Tyr Val
755	760	765
Ile Ala Thr Ala Pro Asn Met	Phe Asn Val Asn Asp Val	Leu Gly Val
770	775	780
Tyr Ser Pro His Pro Tyr Glu	Gln Glu Val Ser Ala Leu	Gly Gly Ile
785	790	795
		800

Pro	Tyr	Ser	Gln	Ile	Tyr	Gly	Trp	Tyr	Arg	Val	Asn	Phe	Gly	Val	Ile
				805					810					815	
Asp	Glu	Arg	Leu	His	Arg	Asn	Arg	Glu	Tyr	Arg	Asp	Arg	Tyr	Tyr	Arg
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Asn	Leu	Asn	Ile	Ala	Pro	Ala	Glu	Asp	Gly	Tyr	Arg	Leu	Ala	Gly	Phe
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Pro	Pro	Asp	His	Gln	Ala	Trp	Arg	Glu	Glu	Pro	Trp	Ile	His	His	Ala
	850					855					860				
Pro	Gln	Gly	Cys	Gly	Asn	Ser	Ser	Arg	Thr	Ile	Thr	Asp	Asp	Thr	Cys
865					870					875				880	
Asn	Glu	Glu	Thr	Gln	Asn	Leu	Ser	Thr	Ile	Tyr	Leu	Arg	Lys	Tyr	Gln
			885						890					895	
Ser	Lys	Val	Lys	Arg	Gln	Ile	Phe	Ser	Asp	Tyr	Gln	Ser	Glu	Val	Asp
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<210> 9

<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 9

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acgccgttca atgtcgagca ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
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<210> 10

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 10

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      20              25              30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      35              40              45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
      50              55              60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65              70              75              80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
      85              90              95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
      100             105             110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
      115             120             125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130             135             140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145             150             155             160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
      165             170             175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
      180             185             190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
      195             200             205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
      210             215             220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225             230             235             240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
      245             250             255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
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305                      310                      315                      320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
      325                      330                      335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
      340                      345                      350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
      355                      360                      365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
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Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385                      390                      395                      400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
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Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
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Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
      435                      440                      445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
      450                      455                      460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                      470                      475                      480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
      485                      490                      495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
      500                      505                      510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
      515                      520                      525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
      530                      535                      540
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Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser

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Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Ala	Ser	Asn	Pro	Ser	Pro	Gln
	610		615		620										
Tyr	Ser	Trp	Arg	Ile	Asn	Gly	Ile	Pro	Gln	Gln	His	Thr	Gln	Val	Leu
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Phe	Ile	Ala	Lys	Ile	Thr	Pro	Asn	Asn	Asn	Gly	Thr	Tyr	Ala	Cys	Phe
	645		650		655										
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Ser	Ile
	660		665		670										
Thr	Val	Ser	Ala	Ser	Gly	Thr	Leu	Asp	Ala	Pro	Gln	Ser	Ile	Thr	Glu
	675		680		685										
Leu	Cys	Ser	Glu	Tyr	Arg	Asn	Thr	Gln	Ile	Tyr	Thr	Ile	Asn	Asp	Lys
	690		695		700										
Ile	Leu	Ser	Tyr	Thr	Glu	Ser	Met	Ala	Gly	Lys	Arg	Glu	Met	Val	Ile
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Ile	Thr	Phe	Lys	Ser	Gly	Ala	Thr	Phe	Gln	Val	Glu	Val	Pro	Gly	Ser
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Gln	His	Ile	Asp	Ser	Gln	Lys	Lys	Ala	Ile	Glu	Arg	Met	Lys	Asp	Thr
	740		745		750										
Leu	Arg	Ile	Thr	Tyr	Leu	Thr	Glu	Thr	Lys	Ile	Asp	Lys	Leu	Cys	Val
	755		760		765										
Trp	Asn	Asn	Lys	Thr	Pro	Asn	Ser	Ile	Ala	Ala	Ile	Ser	Met	Glu	Asn
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<210> 11

<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAopt-LTB fusion

<400> 11

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gccacaaca gcgacaccgg cctgaaccgc accaccgtga ccaccatcac cgtgtacgcc 960
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cccaagccca gcatcagcag caacaacagc aagcccggtg aggacaagga cgccgtggcc 1560
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cccgacagca gctacctgag cggcgccaac ctgaacctga gctgccacag cgccagcaac 1860
cccagcccc agtacagctg gcgcatcaac ggcatcccc agcagcacac ccagggtgctg 1920
ttcatcgcca agatcacccc caacaacaac ggcacctacg cctgcttcgt gagcaacctg 1980
gccaccggcc gcaacaacag catcgtgaag agcatcaccg tgagcgccag cggcacctct 2040
agagctcccc agactattac agaactatgt tcggaatatc gcaacacaca aatatatacg 2100
ataaatgaca agatactatc atatacggaa tcgatggcag gcaaaagaga aatggttatc 2160

```

```

attacattta agagcggcga aacatttcag gtcgaagtcc cgggcagtca acatatagac 2220
tcccagaaaa aagccattga aaggatgaag gacacattaa gaatcacata tctgaccgag 2280
accaaatttg ataaattatg tgtatggaat aataaaaccc ccaattcaat tgcggcaatc 2340
agtatggaaa actag                                     2355

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<210> 12

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAopt-LTBopt fusion

<400> 12

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accgccagcc tgctgacctt ctggaacccc cccaccaccg ccaagctgac catcgagagc 120
accccccttca acgtggccga gggcaaggag gtgctgctgc tgggtgcacaa cctgccccag 180
cacctgttcg gctacagctg gtacaagggc gagcgcgtgg acggcaaccg ccagatcatc 240
ggctacgtga tcggcaccca gcaggccacc cccggccccg cctacagcgg ccgcgagatc 300
atctacccca acgccagcct gctgatccag aacatcatcc agaacgacac cggtttctac 360
accctgcacg tgatcaagag cgacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccgccagc tgcccgaagg cagcatcagc agcaacaaca gcaagcccgt ggaggacaag 480
gacgccgtgg ccttcacctg cgagcccagc acccaggacg ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccgt gagccccccg ctgcagctga gcaacggcaa ccgcaccctg 600
accctgttca acgtgaccgc caacgacacc gccagctaca agtgcgagac ccagaacccc 660
gtgagcgccc gccgcagcga cagcgtgatc ctgaacgtgc tgtacggccc cgacgcccc 720
accatcagcc ccctgaacac cagctaccgc agcggcgaga acctgaacct gagctgccac 780
gccgccagca accccccgc ccagtacagc tggttcgtga acggcacctt ccagcagagc 840
accaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta cacctgccag 900
gccacaaca gcgacaccgg cctgaaccgc accaccgtga ccacctcac cgtgtacgcc 960
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gtggccctga cctgcgagcc cgagatccag aacaccacct acctgtggtg ggtgaacaac 1080
cagagcctgc ccgtgagccc ccgcctgcag ctgagcaacg acaaccgcac cctgaccctg 1140
ctgagcgtga cccgcaacga cgtgggcccc tacgagtgcg gcatccagaa cgagctgagc 1200
gtggaccaca gcgaccccgat gatcctgaac gtgctgtacg gccccgacga cccaccatc 1260
agccccagct acacctacta ccgccccggc gtgaacctga gcctgagctg ccacgccgcc 1320
agcaaccccc ccgcccagta cagctggctg atcgacggca acatccagca gcacaccag 1380

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gagctgttca tcagcaacat caccgagaag aacagcggcc tgtacacctg ccaggccaac 1440
aacagcgcca gcggccacag ccgcaccacc gtgaagacca tcaccgtgag cgccgagctg 1500
cccaagccca gcatcagcag caacaacagc aagcccgtgg aggacaagga cgccgtggcc 1560
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cccgacagca gctacctgag cggcgccaac ctgaacctga gctgccacag cgccagcaac 1860
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ttcatcgcca agatcacccc caacaacaac ggacacctag cctgcttcgt gagcaacctg 1980
gccaccggcc gcaacaacag catcgtgaag agcatcaccg tgagcgccag cggcacctct 2040
agagcccccc agagcatcac cgagctgtgc agcgagtacc ggaacaccca gatctacacc 2100
atcaacgaca agatcctgag ctacaccgag agcatggccg gcaagaggga gatggtgatc 2160
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agccagaaga aggccatcga gcggatgaag gacaccctgc ggatcaccta cctcaccgag 2280
accaagatcg acaagctgtg cgtgtggaac aacaagacc ccaacagcat cgccgccatc 2340
agcatggaga attgataa                                     2358

```

<210> 13

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEAopt-LTBopt fusion

<400> 13

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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
 1             5             10            15
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20             25            30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      35             40            45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
      50             55            60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65             70             75            80

```

Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser	85	90	95
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile	100	105	110
Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp	115	120	125
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu	130	135	140
Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys	145	150	155
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr	165	170	175
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln	180	185	190
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn	195	200	205
Asp	Thr	Ala	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Ala	Arg	210	215	220
Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro	225	230	235
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn	245	250	255
Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	Trp	Phe	260	265	270
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn	275	280	285
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala	His	Asn	Ser	290	295	300
Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr	Val	Tyr	Ala	305	310	315
Glu	Pro	Pro	Lys	Pro	Phe	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	325	330	335
Asp	Glu	Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Ile	Gln	Asn	Thr	340	345	350
Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	355	360	365
Leu	Gln	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Leu	Leu	Ser	Val	Thr			

370	375	380	
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser			
385	390	395	400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp			
405	410	415	
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn			
420	425	430	
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser			
435	440	445	
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile			
450	455	460	
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn			
465	470	475	480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val			
485	490	495	
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro			
500	505	510	
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln			
515	520	525	
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser			
530	535	540	
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn			
545	550	555	560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser			
565	570	575	
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly			
580	585	590	
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly			
595	600	605	
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln			
610	615	620	
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu			
625	630	635	640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe			
645	650	655	
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile			
660	665	670	

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Thr Val Ser Ala Ser Gly Thr Ser Arg Ala Pro Gln Ser Ile Thr Glu
      675                      680                      685
Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys
      690                      695                      700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile
705                      710                      715                      720
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser
      725                      730                      735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
      740                      745                      750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val
      755                      760                      765
Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
      770                      775                      780

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<210> 14

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEAopt-LTBopt fusion

<400> 14

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accgccagcc tgctgacctt ctggaacccc cccaccaccg cccagctgac catcgagagc 120
cgccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
agctgctgta tccgcaccca gcagatcacc cccggccccg cccacagcgg ccgcgagacc 300
atcgacttca acgccagcct gctgatccac aacgtgacct agagcgacac cggcagctac 360
accatccagg tgatcaagga ggacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccgccagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccggt ggaggacaag 480
gacgccgtgg ccctgacctg cgagccccgag acccaggaca ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccgt gagcccccg ctaggagctga gcagcgacaa ccgcacctg 600
accgtgttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
gtgagcgtgc gccgcagcga ccccgtagac ctgaacgtgc tgtacggccc cgacgcccc 720

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accatcagcc ccctgaacac cccctaccgc gccggcgaga acctgaacct gacctgccac 780
gccgccagca accccaccgc ccagtacttc tggttcgtga acggcacctt ccagcagagc 840
accagagagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta catgtgccag 900
gccacaaca gcgccaccgg cctgaaccgc accaccgtga ccgccatcac cgtgtacgcc 960
gagctgccc aagccctacat caccagcaac aacagcaacc ccatcgagga caaggacgcc 1020
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cagagcctga gcgtgagcag ccgcctggag ctgagcaacg acaaccgcac cctgaccgtg 1140
ttcaacatcc cccgcaacga caccaccttc tacgagtgcg agaccagaa ccccgtagc 1200
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gagctgttca tccccaacat caccgtgaac aacagcggca gctacatgtg ccaggccac 1440
aacagcgcca ccggcctgaa ccgcaccacc gtgaccgcca tcaccgtgta cgtggagctg 1500
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cccagcccc agtacagctg gctgatcaac ggcacctgc gccagcacac ccagggtgctg 1920
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gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040
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atcaccttca agagcggcgc caccttccag gtggaggtgc ccggcagcca gcacatcgac 2220
agccagaaga aggccatcga gcggatgaag gacacctgc ggatcaccta cctcaccgag 2280
accaagatcg acaagctgtg cgtgtggaac aacaagacc ccaacagcat cgccgccatc 2340
agcatggaga attgataa 2358

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<210> 15

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEAopt-LTBopt fusion

<400> 15

Met	Gly	Ser	Pro	Ser	Ala	Pro	Leu	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
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Thr	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
			20					25					30		
Thr	Ala	Gln	Leu	Thr	Ile	Glu	Ser	Arg	Pro	Phe	Asn	Val	Ala	Glu	Gly
		35					40					45			
Lys	Glu	Val	Leu	Leu	Leu	Ala	His	Asn	Val	Ser	Gln	Asn	Leu	Phe	Gly
	50					55				60					
Tyr	Ile	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Ala	Ser	Arg	Arg	Ile	Gly
65				70					75					80	
Ser	Cys	Val	Ile	Arg	Thr	Gln	Gln	Ile	Thr	Pro	Gly	Pro	Ala	His	Ser
			85					90					95		
Gly	Arg	Glu	Thr	Ile	Asp	Phe	Asn	Ala	Ser	Leu	Leu	Ile	His	Asn	Val
			100					105					110		
Thr	Gln	Ser	Asp	Thr	Gly	Ser	Tyr	Thr	Ile	Gln	Val	Ile	Lys	Glu	Asp
		115				120						125			
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
	130					135					140				
Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	Asp	Lys
145				150					155					160	
Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr	Thr	Tyr
			165						170				175		
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Glu
			180					185					190		
Leu	Ser	Ser	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro	Arg	Asn
		195				200						205			
Asp	Thr	Thr	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Val	Arg
	210					215					220				
Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro
225				230					235					240	
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn	Leu	Asn
			245					250					255		
Leu	Thr	Cys	His	Ala	Ala	Ser	Asn	Pro	Thr	Ala	Gln	Tyr	Phe	Trp	Phe
		260						265				270			
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn
		275					280					285			

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Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290                               295                   300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
305                               310                   315                   320
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
                               325                   330                   335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
                               340                   345                   350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
                               355                   360                   365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
                               370                   375                   380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
385                               390                   395                   400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
                               405                   410                   415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
                               420                   425                   430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
                               435                   440                   445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
                               450                   455                   460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
465                               470                   475                   480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
                               485                   490                   495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
                               500                   505                   510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
                               515                   520                   525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
                               530                   535                   540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
545                               550                   555                   560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
                               565                   570                   575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly

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580	585	590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly		
595	600	605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln		
610	615	620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu		
625	630	635
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe		
645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile		
660	665	670
Ser Val Ser Ser Gly Asp Ser Ser Arg Ala Pro Gln Ser Ile Thr Glu		
675	680	685
Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys		
690	695	700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile		
705	710	715
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser		
725	730	735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr		
740	745	750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val		
755	760	765
Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn		
770	775	780

<210> 16

<211> 2118

<212> DNA

<213> Macaca mulatta

<400> 16

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acagcctcac ttctaacctt ctggaacccg cccaccactg cccagctcac tattgaatcc 120
aggccgttca atgttgacaga ggggaaggag gttcttctac ttgcccacaa tgtgtcccag 180
aatctttttg gctacatttg gtacaaggga gaaagagtgg atgccagccg tcgaattgga 240

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tcatgtgtaa taagaactca acaaattacc ccaggggcccg cacacagcgg tcgagagaca 300
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accatacaag tcataaagga agatcttgtg aatgaagaag caactggcca gttccgggta 420
taccgggagc tgcccaagcc ctacatctcc agcaacaact ccaaccccggt ggaggacaag 480
gatgctgtgg ccttaacctg tgaacctgag actcaggaca caacctacct gtgggtgggta 540
aacaatcaga gcctcccggg cagtcccagg ctggagctgt ccagtgacaa caggaccctc 600
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gctaccgggtc gcaataactc catagtcaag aacatctcag tctcctctgg cgattcagca 2040
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2118

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<210> 17

<211> 2118

<212> DNA

<213> Macaca mulatta

<400> 17

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ggggttgctc tgatgtag

2118

<210> 18

<211> 705

<212> PRT

<213> Macaca mulatta

<400> 18

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 Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
 50 55 60
 Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
 65 70 75 80
 Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
 85 90 95
 Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
 100 105 110
 Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195 200 205
 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro

225		230		235		240									
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn	Leu	Asn
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Leu	Thr	Cys	His	Ala	Ala	Ser	Asn	Pro	Thr	Ala	Gln	Tyr	Phe	Trp	Phe
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Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn
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Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Met	Cys	Gln	Ala	His	Asn	Ser
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Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Ile	Glu
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Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser	Ser	Arg
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Leu	Glu	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro
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Val	Arg	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp
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Ala	Pro	Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn
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Leu	Asn	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Ala	Ala	Gln	Tyr	Ser
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Trp	Phe	Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile
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Pro	Asn	Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Met	Cys	Gln	Ala	His
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Asn	Ser	Ala	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Ala	Ile	Thr	Val
					485					490					495
Tyr	Val	Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro
					500					505				510	
Ile	Glu	Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Val	Ala	Glu
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Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
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Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
565                      570                      575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
580                      585                      590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
595                      600                      605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
610                      615                      620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
625                      630                      635                      640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
645                      650                      655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
660                      665                      670
Ser Val Ser Ser Gly Asp Ser Ala Pro Gly Ser Ser Gly Leu Ser Ala
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Arg Ala Thr Val Gly Ile Ile Ile Gly Met Leu Val Gly Val Ala Leu
690                      695                      700
Met
705

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<210> 19

<211> 705

<212> PRT

<213> Macaca mulatta

<400> 19

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Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
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20                      25                      30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly

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	35		40		45												
Lys	Glu	Val	Leu	Leu	Leu	Ala	His	Asn	Val	Ser	Gln	Asn	Leu	Phe	Gly		
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Tyr	Ile	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Ala	Ser	Arg	Arg	Ile	Gly		
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Ser	Cys	Val	Ile	Arg	Thr	Gln	Gln	Ile	Thr	Pro	Gly	Pro	Ala	His	Ser		
				85					90					95			
Gly	Arg	Glu	Thr	Ile	Asp	Phe	Asn	Ala	Ser	Leu	Leu	Ile	His	Asn	Val		
				100				105					110				
Thr	Gln	Ser	Asp	Thr	Gly	Ser	Tyr	Thr	Ile	Gln	Val	Ile	Lys	Glu	Asp		
				115				120					125				
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu		
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Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	Asp	Lys		
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Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr	Thr	Tyr		
				165					170					175			
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Glu		
				180				185					190				
Leu	Ser	Ser	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro	Arg	Asn		
				195				200					205				
Asp	Thr	Thr	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Val	Arg		
				210				215				220					
Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro		
225					230				235					240			
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn	Leu	Asn		
				245					250					255			
Leu	Thr	Cys	His	Ala	Ala	Ser	Asn	Pro	Thr	Ala	Gln	Tyr	Phe	Trp	Phe		
				260				265					270				
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn		
				275				280					285				
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Met	Cys	Gln	Ala	His	Asn	Ser		
				290				295				300					
Ala	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Ala	Ile	Thr	Val	Tyr	Ala		
305					310					315				320			
Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Ile	Glu		
				325					330					335			

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Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
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Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
      355                      360                      365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
      370                      375                      380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
385                      390                      395                      400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
      405                      410                      415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
      420                      425                      430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Phe
      435                      440                      445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
      450                      455                      460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
465                      470                      475                      480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
      485                      490                      495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
      500                      505                      510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
      515                      520                      525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
      530                      535                      540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
545                      550                      555                      560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
      565                      570                      575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
      580                      585                      590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
      595                      600                      605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
      610                      615                      620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu

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625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Asn Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
 Ser Val Ser Ser Gly Asp Ser Ala Pro Gly Ser Ser Gly Leu Ser Ala
 675 680 685
 Arg Ala Thr Val Gly Ile Ile Ile Gly Met Leu Val Gly Val Ala Leu
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 Met
 705

<210> 20
 <211> 702
 <212> PRT
 <213> Homo sapiens

<400> 20
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 35 40 45
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140

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Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
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Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
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Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
                180                185                190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
                195                200                205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
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Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                230                235                240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
                245                250                255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
                260                265                270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
                275                280                285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
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Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305                310                315                320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325                330                335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
                340                345                350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
                355                360                365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
                370                375                380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385                390                395                400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                405                410                415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
                420                425                430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser

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435		440		445											
Trp	Leu	Ile	Asp	Gly	Asn	Ile	Gln	Gln	His	Thr	Gln	Glu	Leu	Phe	Ile
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Ser	Asn	Ile	Thr	Glu	Lys	Asn	Ser	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Asn
465		470		475		480									
Asn	Ser	Ala	Ser	Gly	His	Ser	Arg	Thr	Thr	Val	Lys	Thr	Ile	Thr	Val
		485		490		495									
Ser	Ala	Glu	Leu	Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro
	500			505		510									
Val	Glu	Asp	Lys	Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Ala	Gln
	515			520		525									
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Gly	Gln	Ser	Leu	Pro	Val	Ser
	530			535		540									
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn
545		550		555		560									
Val	Thr	Arg	Asn	Asp	Ala	Arg	Ala	Tyr	Val	Cys	Gly	Ile	Gln	Asn	Ser
	565			570		575									
Val	Ser	Ala	Asn	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asp	Val	Leu	Tyr	Gly
	580			585		590									
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Ser	Ser	Tyr	Leu	Ser	Gly
	595			600		605									
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Ala	Ser	Asn	Pro	Ser	Pro	Gln
	610			615		620									
Tyr	Ser	Trp	Arg	Ile	Asn	Gly	Ile	Pro	Gln	Gln	His	Thr	Gln	Val	Leu
625		630		635		640									
Phe	Ile	Ala	Lys	Ile	Thr	Pro	Asn	Asn	Asn	Gly	Thr	Tyr	Ala	Cys	Phe
	645			650		655									
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Ser	Ile
	660			665		670									
Thr	Val	Ser	Ala	Ser	Gly	Thr	Ser	Pro	Gly	Leu	Ser	Ala	Gly	Ala	Thr
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Val	Gly	Ile	Met	Ile	Gly	Val	Leu	Val	Gly	Val	Ala	Leu	Ile		
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<210> 21

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAoptDOMopt fusion

<400> 21

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<211> 2037

<212> DNA

<213> Artificial Sequence

<220>

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<210> 23

<211> 679

<212> PRT

<213> Artificial Sequence

<220>

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 50 55 60
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
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 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
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Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
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<211> 3426

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-FRC fusion

<400> 24

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<212> DNA

<213> Artificial Sequence

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<223> CEA-FcIgG fusion

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<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LAMP fusion

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<211> 3921

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-HSP70 fusion

<400> 27

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<211> 3585

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-VSVG fusion

<400> 28

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<223> PCR Primer

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<210> 30

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 30

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33

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 31

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<210> 32

<211> 36

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<223> PCR Primer

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<211> 25

<212> DNA

<213> Artificial Sequence

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<220>

<223> PCR Primer

<400> 34

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<210> 35

<211> 37

<212> DNA

<213> Artificial Sequence

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<223> PCR Primer

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<210> 36

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36

<210> 39

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<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 39

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<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 42

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<210> 43
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<220>
 <223> PCR Primer

<400> 43
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<210> 44
 <211> 31
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<220>
 <223> PCR Primer

<400> 44
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<210> 45
 <211> 952
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-Dom fusion

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 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly

35	40	45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly		
50	55	60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile		
65	70	75
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser		
85	90	95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile		
100	105	110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp		
115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys		
145	150	155
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr		
165	170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln		
180	185	190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn		
195	200	205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg		
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Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn		
245	250	255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe		
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Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser		
290	295	300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala		
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Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu		
325	330	335

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Arg	Asn	Asp	Val	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Glu	Leu	Ser				
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Val	Asp	His	Ser	Asp	Pro	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp				
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Asp	Pro	Thr	Ile	Ser	Pro	Ser	Tyr	Thr	Tyr	Tyr	Arg	Pro	Gly	Val	Asn				
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Val	Ser	Ala	Asn	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asp	Val	Leu	Tyr	Gly				
																580	585	590	
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Ser	Ser	Tyr	Leu	Ser	Gly				
																595	600	605	
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Ala	Ser	Asn	Pro	Ser	Pro	Gln				
																610	615	620	
Tyr	Ser	Trp	Arg	Ile	Asn	Gly	Ile	Pro	Gln	Gln	His	Thr	Gln	Val	Leu				

625				630				635				640			
Phe	Ile	Ala	Lys	Ile	Thr	Pro	Asn	Asn	Asn	Gly	Thr	Tyr	Ala	Cys	Phe
645				650				655							
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Ser	Ile
660				665				670							
Thr	Val	Ser	Ala	Ser	Gly	Thr	Ser	Arg	Ser	Thr	Pro	Ile	Pro	Phe	Ser
675				680				685							
Tyr	Ser	Lys	Asn	Leu	Asp	Cys	Trp	Val	Asp	Asn	Glu	Glu	Asp	Ile	Asp
690				695				700							
Val	Ile	Leu	Lys	Lys	Ser	Thr	Ile	Leu	Asn	Leu	Asp	Ile	Asn	Asn	Asp
705				710				715				720			
Ile	Ile	Ser	Asp	Ile	Ser	Gly	Phe	Asn	Ser	Ser	Val	Ile	Thr	Tyr	Pro
725				730				735							
Asp	Ala	Gln	Leu	Val	Pro	Gly	Ile	Asn	Gly	Lys	Ala	Ile	His	Leu	Val
740				745				750							
Asn	Asn	Glu	Ser	Ser	Glu	Val	Ile	Val	His	Lys	Ala	Met	Asp	Ile	Glu
755				760				765							
Tyr	Asn	Asp	Met	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val
770				775				780							
Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Gln	Tyr	Gly	Thr	Asn	Glu	Tyr
785				790				795				800			
Ser	Ile	Ile	Ser	Ser	Met	Lys	Lys	His	Ser	Leu	Ser	Ile	Gly	Ser	Gly
805				810				815							
Trp	Ser	Val	Ser	Leu	Lys	Gly	Asn	Asn	Leu	Ile	Trp	Thr	Leu	Lys	Asp
820				825				830							
Ser	Ala	Gly	Glu	Val	Arg	Gln	Ile	Thr	Phe	Arg	Asp	Leu	Pro	Asp	Lys
835				840				845							
Phe	Asn	Ala	Tyr	Leu	Ala	Asn	Lys	Trp	Val	Phe	Ile	Thr	Ile	Thr	Asn
850				855				860							
Asp	Arg	Leu	Ser	Ser	Ala	Asn	Leu	Tyr	Ile	Asn	Gly	Val	Leu	Met	Gly
865				870				875				880			
Ser	Ala	Glu	Ile	Thr	Gly	Leu	Gly	Ala	Ile	Arg	Glu	Asp	Asn	Asn	Ile
885				890				895							
Thr	Leu	Lys	Leu	Asp	Arg	Cys	Asn	Asn	Asn	Asn	Gln	Tyr	Val	Ser	Ile
900				905				910							
Asp	Lys	Phe	Arg	Ile	Phe	Cys	Lys	Ala	Leu	Asn	Pro	Lys	Glu	Ile	Glu
915				920				925							

Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp
 930 935 940

Gly Asn Pro Leu Arg Tyr Asp Thr
 945 950

<210> 46

<211> 907

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-FcIgG fusion

<400> 46

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
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 Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
 20 25 30
 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175

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Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
      180                      185                      190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
      195                      200                      205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
      210                      215                      220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
      225                      230                      235                      240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
      245                      250                      255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
      260                      265                      270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
      275                      280                      285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
      290                      295                      300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
      305                      310                      315                      320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
      325                      330                      335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
      340                      345                      350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
      355                      360                      365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
      370                      375                      380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
      385                      390                      395                      400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
      405                      410                      415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
      420                      425                      430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
      435                      440                      445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
      450                      455                      460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn

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465		470		475		480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val						
	485		490		495	
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro						
	500		505		510	
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln						
	515		520		525	
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser						
	530		535		540	
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn						
545		550		555		560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser						
	565		570		575	
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly						
	580		585		590	
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly						
	595		600		605	
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln						
	610		615		620	
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu						
625		630		635		640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe						
	645		650		655	
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile						
	660		665		670	
Thr Val Ser Ala Ser Gly Thr Ser Arg Lys Thr His Thr Cys Pro Pro						
	675		680		685	
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro						
	690		695		700	
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr						
705		710		715		720
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn						
	725		730		735	
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg						
	740		745		750	
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val						
	755		760		765	

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 770 775 780
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 785 790 795 800
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 805 810 815
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 820 825 830
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 835 840 845
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 850 855 860
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 865 870 875 880
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 885 890 895
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 900 905

<210> 47

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<223> DOM

<400> 47

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 gaagatatag atgttatatt aaaaaagagt acaattttta attagatat taataatgat 120
 attatatcag atatatctgg gtttaattca tctgtaataa catatccaga tgctcaattg 180
 gtgcccggaa taaatggcaa agcaatacat ttagtaaaca atgaatcttc tgaagttata 240
 gtgcataaag ctatggatat tgaatataat gatatgttta ataattttac cgtaggcttt 300
 tgggttgaggg ttcttaaagt atctgctagt catttagaac aatatggcac aaatgagtat 360
 tcaataatta gctctatgaa aaaacatagt ctatcaatag gatctgggtg gagtgtatca 420
 cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 480

acttttaggg atttacctga taaatttaaat gcttatttag caaataaatg ggtttttata 540
 actattacta atgatatgatt atcttctgct aatttgtata taaatggagt acttatggga 600
 agtgcagaaa ttactggttt aggagctatt agagaggata ataataaac attaaaacta 660
 gatagatgta ataataataa tcaatacgtt tctattgata aatttaggat attttgcaaa 720
 gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aaccttttta 780
 agagacttct ggggaaaccc ttacgatat gatacagata ggtag 825

<210> 48

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> DOM

<400> 48

Asp	Ser	Thr	Pro	Ile	Pro	Phe	Ser	Tyr	Ser	Lys	Asn	Leu	Asp	Cys	Trp
1				5					10					15	
Val	Asp	Asn	Glu	Glu	Asp	Ile	Asp	Val	Ile	Leu	Lys	Lys	Ser	Thr	Ile
			20					25					30		
Leu	Asn	Leu	Asp	Ile	Asn	Asn	Asp	Ile	Ile	Ser	Asp	Ile	Ser	Gly	Phe
			35				40					45			
Asn	Ser	Ser	Val	Ile	Thr	Tyr	Pro	Asp	Ala	Gln	Leu	Val	Pro	Gly	Ile
			50			55				60					
Asn	Gly	Lys	Ala	Ile	His	Leu	Val	Asn	Asn	Glu	Ser	Ser	Glu	Val	Ile
65				70						75				80	
Val	His	Lys	Ala	Met	Asp	Ile	Glu	Tyr	Asn	Asp	Met	Phe	Asn	Asn	Phe
			85						90				95		
Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu
			100					105					110		
Glu	Gln	Tyr	Gly	Thr	Asn	Glu	Tyr	Ser	Ile	Ile	Ser	Ser	Met	Lys	Lys
			115					120					125		
His	Ser	Leu	Ser	Ile	Gly	Ser	Gly	Trp	Ser	Val	Ser	Leu	Lys	Gly	Asn
			130				135					140			
Asn	Leu	Ile	Trp	Thr	Leu	Lys	Asp	Ser	Ala	Gly	Glu	Val	Arg	Gln	Ile
145				150						155				160	
Thr	Phe	Arg	Asp	Leu	Pro	Asp	Lys	Phe	Asn	Ala	Tyr	Leu	Ala	Asn	Lys

	165		170		175										
Trp	Val	Phe	Ile	Thr	Ile	Thr	Asn	Asp	Arg	Leu	Ser	Ser	Ala	Asn	Leu
	180		185		190										
Tyr	Ile	Asn	Gly	Val	Leu	Met	Gly	Ser	Ala	Glu	Ile	Thr	Gly	Leu	Gly
	195		200		205										
Ala	Ile	Arg	Glu	Asp	Asn	Asn	Ile	Thr	Leu	Lys	Leu	Asp	Arg	Cys	Asn
	210		215		220										
Asn	Asn	Asn	Gln	Tyr	Val	Ser	Ile	Asp	Lys	Phe	Arg	Ile	Phe	Cys	Lys
225			230		235										240
Ala	Leu	Asn	Pro	Lys	Glu	Ile	Glu	Lys	Leu	Tyr	Thr	Ser	Tyr	Leu	Ser
	245		250		255										
Ile	Thr	Phe	Leu	Arg	Asp	Phe	Trp	Gly	Asn	Pro	Leu	Arg	Tyr	Asp	Thr
	260		265		270										
Asp	Arg														

<210> 49

<211> 2857

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-DOM fusion

<400> 49

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atggagtctc cctcggtccc tccccacaga tgggtgcatcc cctggcagag gctcctgctc 60
acagcctcac ttctaacctt ctggaacccg cccaccactg ccaagctcac tattgaatcc 120
acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggtccc catacagtgg tcgagagata 300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
taccgggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgtg ggaggacaag 480
gatgctgtgg cttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccgtt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaacca 660

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gtgagtgccca ggcgcagtgga ttcagtcacac ctgaatgtcc tctatggccc ggatgcccc 720
accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctctgccac 780
gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgccaa 900
gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
gagccacca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg ggtaaataat 1080
cagagcctcc cggtcagtc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140
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gttgaccaca gcgacccagt catcctgaat gtcctctatg gcccagacga cccaccatt 1260
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cccaagccct ccatctccag caacaactcc aaaccctgg aggacaagga tgctgtggcc 1560
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cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 2520
acttttaggg atttacctga taaatttaat gcttatttag caaataaatg ggtttttata 2580
actattacta atgatagatt atcttctgct aatttgtata taaatggagt acttatggga 2640
agtgcagaaa ttactgggtt aggagctatt agagaggata ataataaac attaaaacta 2700
gatagatgta ataataataa tcaatacgtt tctattgata aatttaggat attttgcaaa 2760
gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aaccttttta 2820
agagacttct ggggaaaccc ttacgatat gatatag 2857

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<210> 50

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 50

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cgcccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
aacctgttcg gctacatctg gtacaagggc gagcgctgg acgccagccg ccgcatcggc 240
agctgctgta tccgcaccca gcagatcacc cccggccccg cccacagcgg ccgcgagacc 300
atcgacttca acgccagcct gctgatccac aacgtgacce agagcgacac cggcagctac 360
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taccgccagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccggt ggaggacaag 480
gacgccgtgg ccctgacctg cgagccccgag acccaggaca ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccgt gagcccccg ctaggagctga gcagcgacaa ccgcaccctg 600
accgtgttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
gtgagcgtgc gccgcagcga ccccgtagcc ctgaacgtgc tgtacggccc cgacgcccc 720
accatcagcc ccctgaacac cccctaccgc gccggcgaga acctgaacct gacctgccac 780
gccgccagca accccaccgc ccagtaactt tggttcgtga acggcacctt ccagcagagc 840
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gtgcgccga gcgaccccg gacctgaac gtgctgtacg gccccgacgc cccaccatc 1260
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aacagcgcca ccggcctgaa ccgcaccacc gtgaccgcca tcaccgtgta cgtggagctg 1500
cccaagccct acatcagcag caacaacagc aaccccatcg aggacaagga cgcctgacc 1560
ctgacctgcg agccccgtggc cgagaacacc acctacctgt ggtgggtgaa caaccagagc 1620

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ctgagcgtga gccccgcct gcagctgagc aacggcaacc gcatcctgac cctgctgagc 1680
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gaggacatcg acgtgatcct gaagaagagc accatcctga acctggacat caacaacgac 2160
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gacagatgca acaacaacaa ccagtacgtg agcatcgaca agttccggat cttctgcaag 2760
gccctgaacc ccaaggagat cgagaagctg tacaccagct acctgagcat caccttcctg 2820
agagacttct ggggcaaccc cctgagatac gacacctag 2859

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<210> 51

<211> 952

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 51

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Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
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Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
          20             25             30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
          35             40             45

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Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
 50 55 60
 Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
 65 70 75 80
 Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
 85 90 95
 Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
 100 105 110
 Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195 200 205
 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
 245 250 255
 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290 295 300
 Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
 325 330 335
 Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr

			340					345					350			
Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser	Ser	Arg	
		355					360					365				
Leu	Glu	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro	
	370					375					380					
Arg	Asn	Asp	Thr	Thr	Phe	Tyr	Glu	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	
385					390					395					400	
Val	Arg	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	
				405					410					415		
Ala	Pro	Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn	
		420					425					430				
Leu	Asn	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Ala	Ala	Gln	Tyr	Ser	
	435					440					445					
Trp	Phe	Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	
	450					455					460					
Pro	Asn	Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Met	Cys	Gln	Ala	His	
465					470					475					480	
Asn	Ser	Ala	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Ala	Ile	Thr	Val	
				485					490					495		
Tyr	Val	Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro	
		500					505					510				
Ile	Glu	Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Val	Ala	Glu	
	515					520					525					
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser	
	530					535					540					
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Ile	Leu	Thr	Leu	Leu	Ser	
545					550					555					560	
Val	Thr	Arg	Asn	Asp	Thr	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Ser	
				565					570					575		
Glu	Ser	Ala	Lys	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Thr	Tyr	Gly	
		580					585					590				
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Leu	Ser	Tyr	Arg	Ser	Gly	
	595					600					605					
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Asp	Ser	Asn	Pro	Ser	Pro	Gln	
	610					615					620					
Tyr	Ser	Trp	Leu	Ile	Asn	Gly	Thr	Leu	Arg	Gln	His	Thr	Gln	Val	Leu	
625					630					635					640	

Phe	Ile	Ser	Lys	Ile	Thr	Ser	Asn	Asn	Ser	Gly	Ala	Tyr	Ala	Cys	Phe	645	650	655
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Asn	Ile	660	665	670
Ser	Val	Ser	Ser	Gly	Asp	Ser	Ser	Arg	Ser	Thr	Pro	Ile	Pro	Phe	Ser	675	680	685
Tyr	Ser	Lys	Asn	Leu	Asp	Cys	Trp	Val	Asp	Asn	Glu	Glu	Asp	Ile	Asp	690	695	700
Val	Ile	Leu	Lys	Lys	Ser	Thr	Ile	Leu	Asn	Leu	Asp	Ile	Asn	Asn	Asp	705	710	715
Ile	Ile	Ser	Asp	Ile	Ser	Gly	Phe	Asn	Ser	Ser	Val	Ile	Thr	Tyr	Pro	725	730	735
Asp	Ala	Gln	Leu	Val	Pro	Gly	Ile	Asn	Gly	Lys	Ala	Ile	His	Leu	Val	740	745	750
Asn	Asn	Glu	Ser	Ser	Glu	Val	Ile	Val	His	Lys	Ala	Met	Asp	Ile	Glu	755	760	765
Tyr	Asn	Asp	Met	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	770	775	780
Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Gln	Tyr	Gly	Thr	Asn	Glu	Tyr	785	790	795
Ser	Ile	Ile	Ser	Ser	Met	Lys	Lys	His	Ser	Leu	Ser	Ile	Gly	Ser	Gly	805	810	815
Trp	Ser	Val	Ser	Leu	Lys	Gly	Asn	Asn	Leu	Ile	Trp	Thr	Leu	Lys	Asp	820	825	830
Ser	Ala	Gly	Glu	Val	Arg	Gln	Ile	Thr	Phe	Arg	Asp	Leu	Pro	Asp	Lys	835	840	845
Phe	Asn	Ala	Tyr	Leu	Ala	Asn	Lys	Trp	Val	Phe	Ile	Thr	Ile	Thr	Asn	850	855	860
Asp	Arg	Leu	Ser	Ser	Ala	Asn	Leu	Tyr	Ile	Asn	Gly	Val	Leu	Met	Gly	865	870	875
Ser	Ala	Glu	Ile	Thr	Gly	Leu	Gly	Ala	Ile	Arg	Glu	Asp	Asn	Asn	Ile	885	890	895
Thr	Leu	Lys	Leu	Asp	Arg	Cys	Asn	Asn	Asn	Asn	Gln	Tyr	Val	Ser	Ile	900	905	910
Asp	Lys	Phe	Arg	Ile	Phe	Cys	Lys	Ala	Leu	Asn	Pro	Lys	Glu	Ile	Glu	915	920	925
Lys	Leu	Tyr	Thr	Ser	Tyr	Leu	Ser	Ile	Thr	Phe	Leu	Arg	Asp	Phe	Trp			

930
Gly Asn Pro Leu Arg Tyr Asp Thr
945

935
950

940

<210> 52

<211> 2359

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-CTBopt fusion

<400> 52

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cgcccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
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taccgccagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccggt ggaggacaag 480
gacgccgtgg ccctgacctg cgagcccagc acccaggaca ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccgt gagccccgcg ctggagctga gcagcgacaa ccgcaccctg 600
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gtgagcgtgc gccgcagcga ccccgtagcc ctgaacgtgc tgtacggccc cgacgcccc 720
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gagctgttca tccccaacat caccgtgaac aacagcggca gctacatgtg ccaggccccc 1440
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gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040
agaaccctc agaacatcac cgatctgtgc gccgagtacc acaacaccca gatctacacc 2100
ctgaacgaca agatcttcag ctacaccgag agcctggccg gcaagagaga gatggccatc 2160
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agccagaaga aggccatcga gcggatgaag gacaccctgc ggatcgcta cctcaccgag 2280
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<210> 53

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-CTBopt fusion

<400> 53

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Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
 1             5             10             15
Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20             25             30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
      35             40             45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
      50             55             60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65             70             75             80

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Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser			
	85	90	95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val			
	100	105	110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp			
	115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu			
	130	135	140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys			
	145	150	155
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr			
	165	170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu			
	180	185	190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn			
	195	200	205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg			
	210	215	220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro			
	225	230	235
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn			
	245	250	255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe			
	260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn			
	275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser			
	290	295	300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala			
	305	310	315
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu			
	325	330	335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr			
	340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg			
	355	360	365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro			

370	375	380	
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser			
385	390	395	400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp			
405	410	415	
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn			
420	425	430	
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser			
435	440	445	
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile			
450	455	460	
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His			
465	470	475	480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val			
485	490	495	
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro			
500	505	510	
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu			
515	520	525	
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser			
530	535	540	
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser			
545	550	555	560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser			
565	570	575	
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly			
580	585	590	
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly			
595	600	605	
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln			
610	615	620	
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu			
625	630	635	640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe			
645	650	655	
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile			
660	665	670	

Ser	Val	Ser	Ser	Gly	Asp	Ser	Ser	Arg	Thr	Pro	Gln	Asn	Ile	Thr	Asp
675				680				685							
Leu	Cys	Ala	Glu	Tyr	His	Asn	Thr	Gln	Ile	Tyr	Thr	Leu	Asn	Asp	Lys
690				695				700							
Ile	Phe	Ser	Tyr	Thr	Glu	Ser	Leu	Ala	Gly	Lys	Arg	Glu	Met	Ala	Ile
705				710				715				720			
Ile	Thr	Phe	Lys	Asn	Gly	Ala	Ile	Phe	Gln	Val	Glu	Val	Pro	Gly	Ser
725				730				735							
Gln	His	Ile	Asp	Ser	Gln	Lys	Lys	Ala	Ile	Glu	Arg	Met	Lys	Asp	Thr
740				745				750							
Leu	Arg	Ile	Ala	Tyr	Leu	Thr	Glu	Ala	Lys	Val	Glu	Lys	Leu	Cys	Val
755				760				765							
Trp	Asn	Asn	Lys	Thr	Pro	His	Ala	Ile	Ala	Ala	Ile	Ser	Met	Ala	Asn
770				775				780							

<210> 54

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> tetanus toxoid peptide

<400> 54

Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala
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Ser	His	Leu	Glu												
20															